

Fig. 1

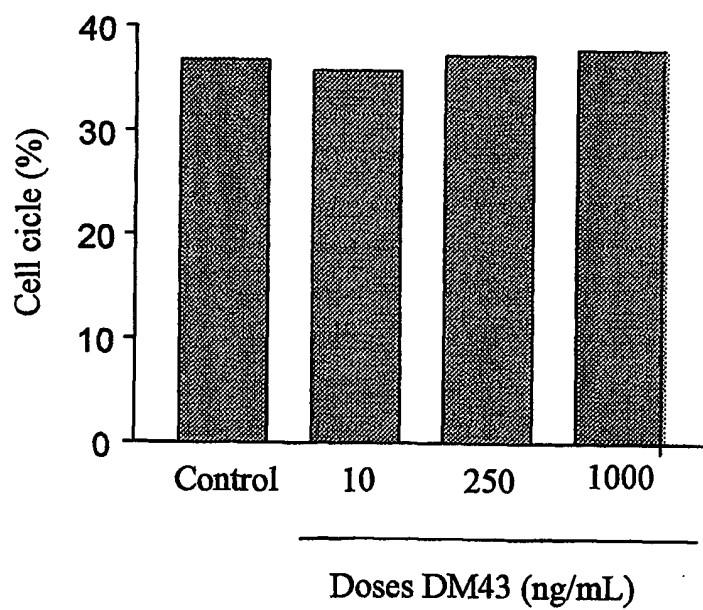


Fig. 2

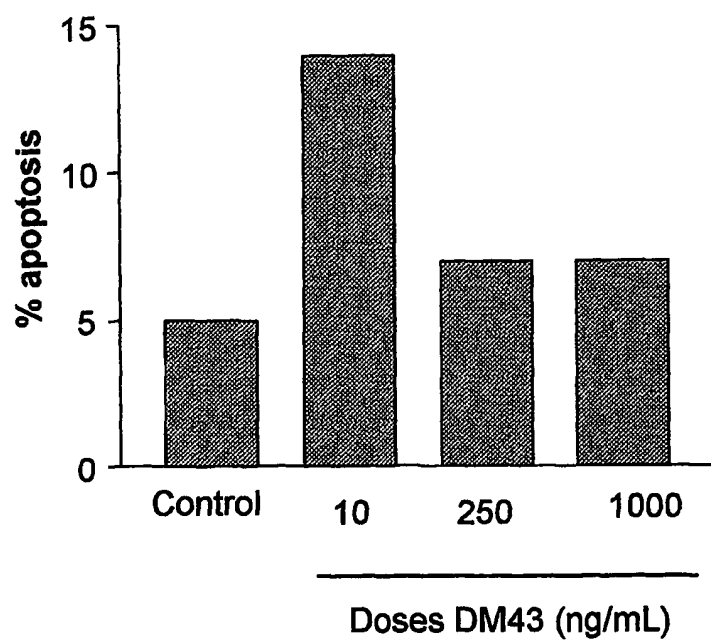


Fig. 3

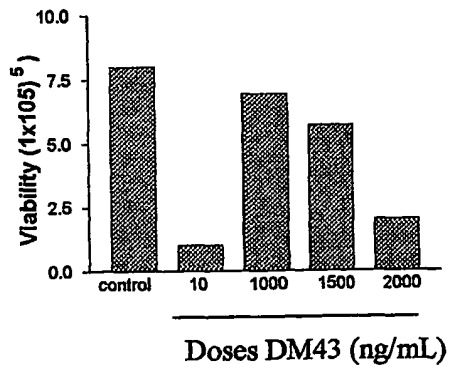


Fig. 4A

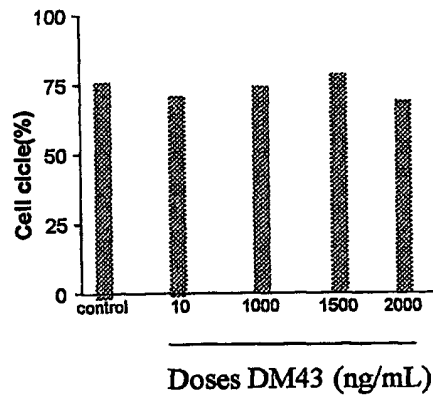


Fig. 4B

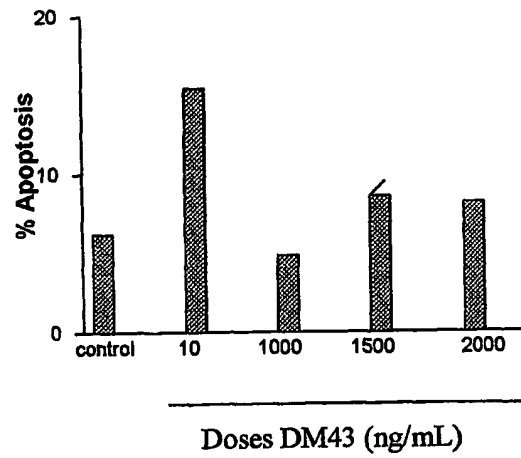
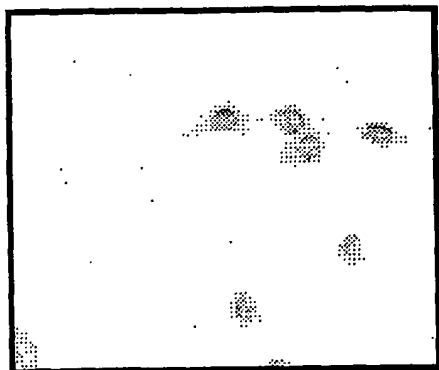
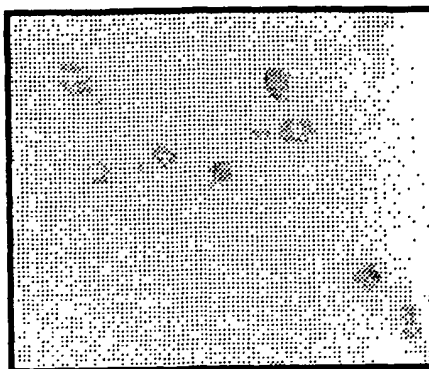


Fig. 4C



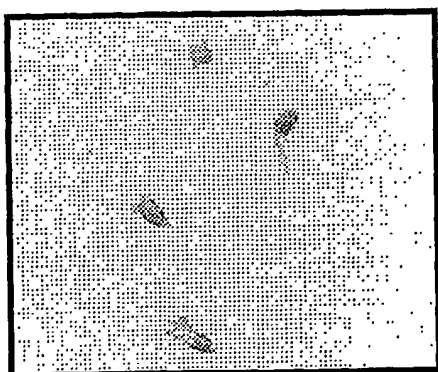
Control

Fig. 5A



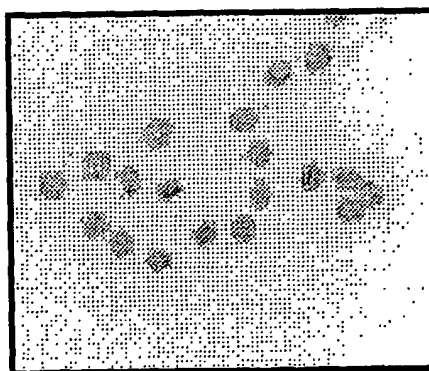
DM43 (10ng/mL)

Fig. 5B



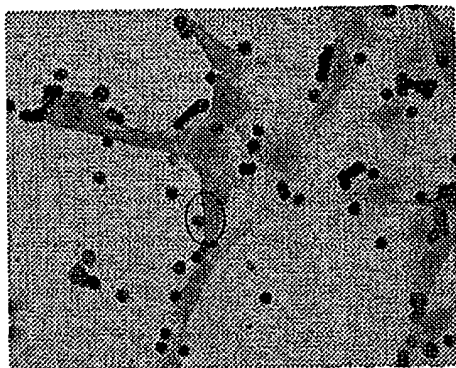
DM 43 (250ng/mL)

Fig. 5C



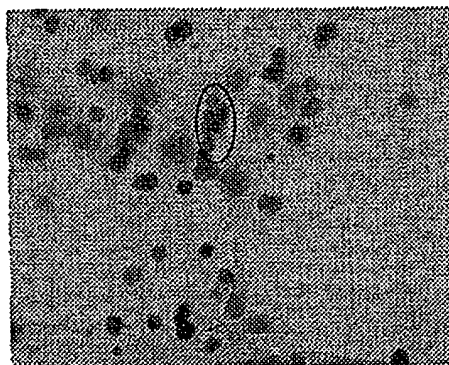
DM43 (1000ng/mL)

Fig. 5D



control

Fig. 6A



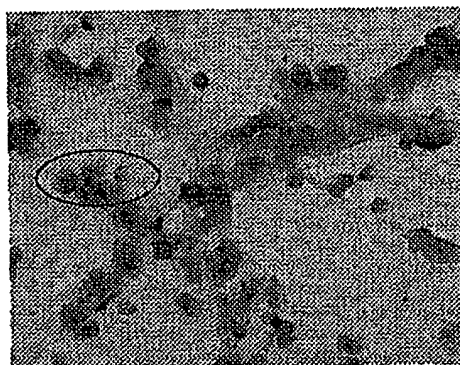
DM43 (10ng/mL)

Fig. 6B



DM 43 (250ng/mL)

Fig. 6C



DM43 (1000ng/mL)

Fig. 6D

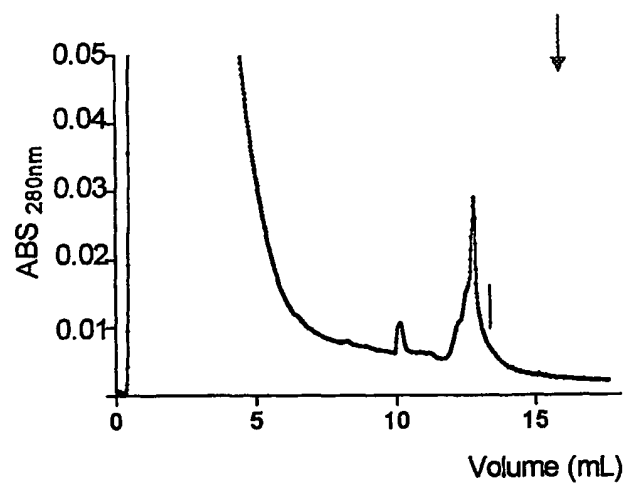


Fig. 7

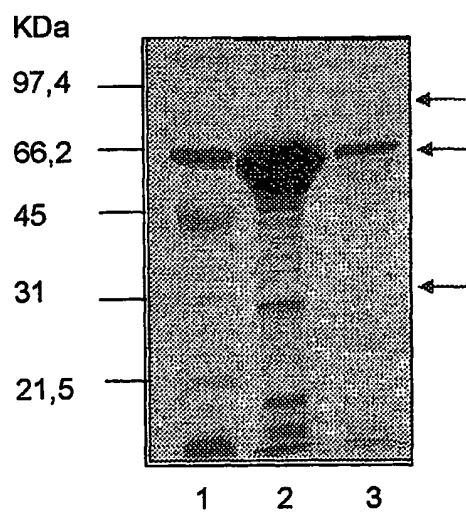


Fig. 8

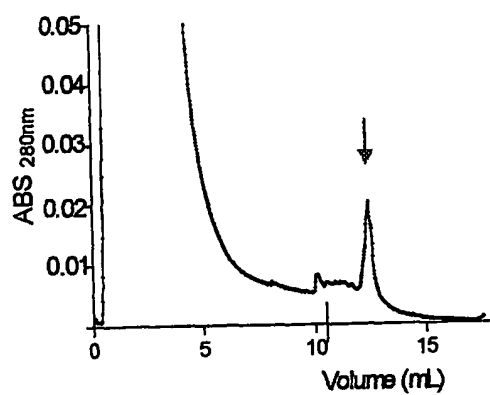


Fig. 9A

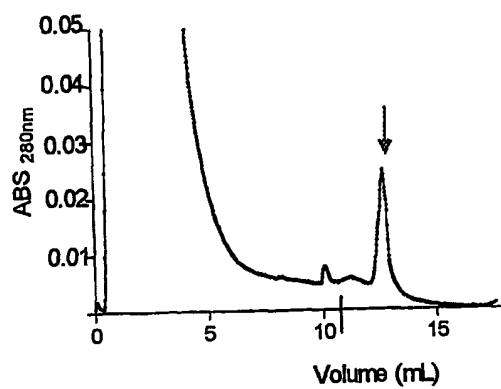


Fig. 9B

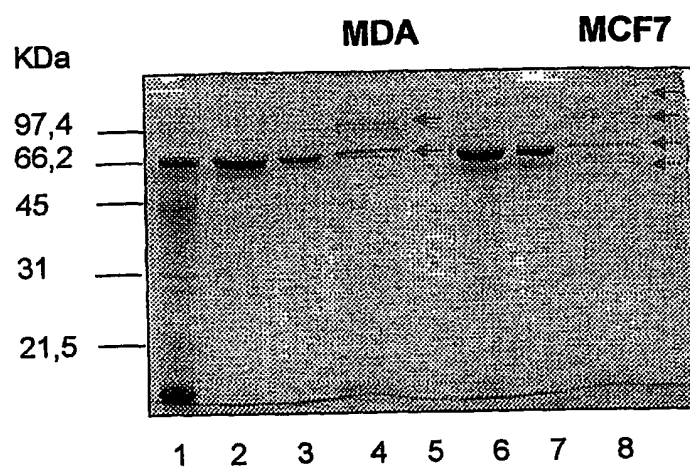


Fig. 10

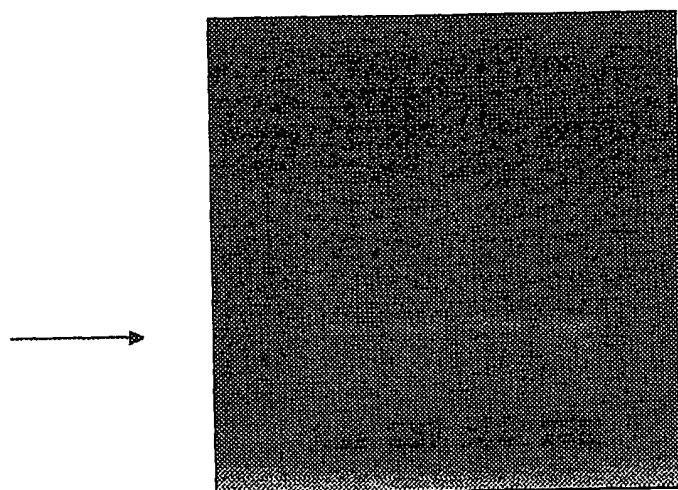


Fig. 11

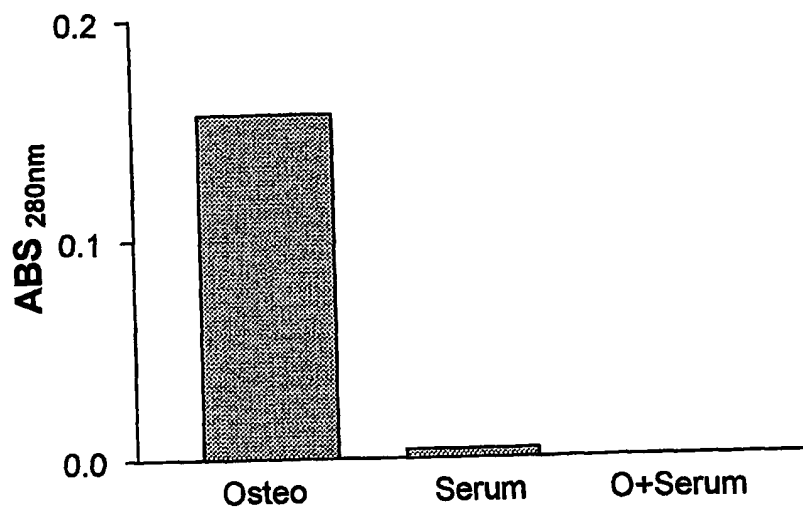


Fig. 12

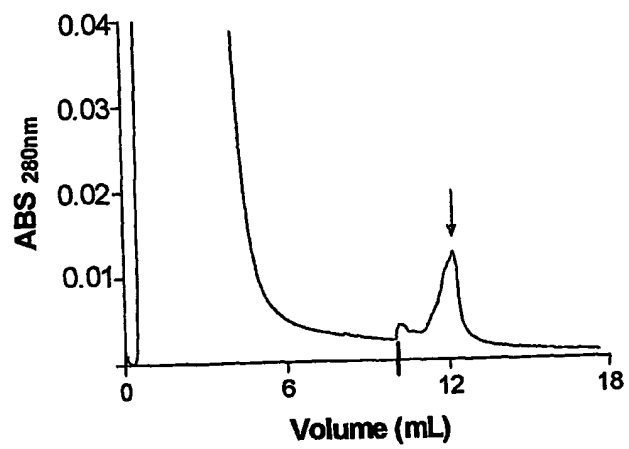


Fig. 13

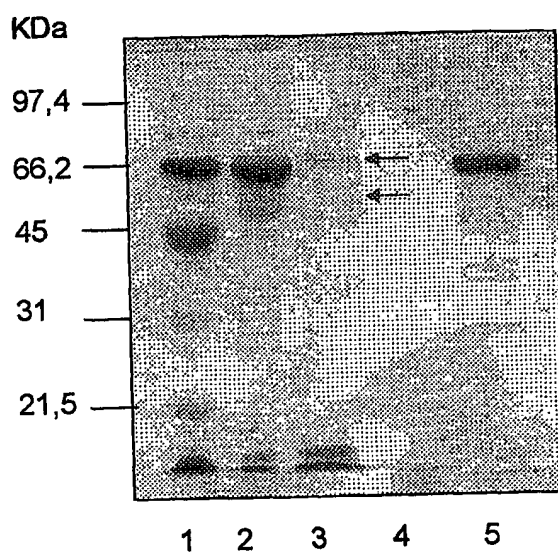


Fig. 14A

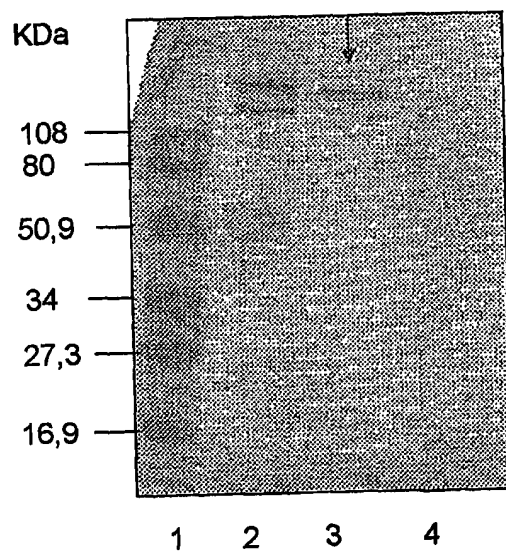


Fig. 14B

TABLE II
MEMBERS OF THE MATRIN Family

Group name	MMP number	EC number	<i>M_r</i> , latent/active	Notes
Collagenase				
Collagenase 1	MMP-1	EC 3.4.24.7	52,000 42,000	Interstitial collagenase
Collagenase 2	MMP-8	EC 3.4.24.34	86,000 64,000	Neutrophil collagenase
Collagenase 3	MMP-13		52,000 42,000	Rodent interstitial collagenase
Collagenase 4	MMP-18		53,000 43,000	<i>Xenopus</i>
Gelatinase				
Gelatinase A	MMP-2	EC 3.4.24.24	72,000 66,000	Type IV collagenase
Gelatinase B	MMP-9	EC 3.4.24.25	92,000 84,000	Type V collagenase
Stromelysin				
Stromelysin 1	MMP-3	EC 3.4.24.17	57,000 45,000	Transin
Stromelysin 2	MMP-10	EC 3.4.24.22	54,000 44,000	Transin-2
Stromelysin 3 ¹	MMP-11	EC 3.4.24.	64,000 46,000	RRKR furin cleavage
Membrane-type				
MT1-MMP	MMP-14		65,000 54,000	Transmembrane domain and RRKR furin cleavage site
MT2-MMP	MMP-15		72,000 60,000	
MT3-MMP	MMP-16		64,000 53,000	
MT4-MMP	MMP-17		57,000 53,000	
Others				
Matrilysin	MMP-7	EC 3.4.25.33	28,000 19,000	Lacks hemopexin
Metalloelastase	MMP-12	EC 3.4.24.65	54,000 23,000	Macrophage elastase
(No trivial name) ²	MMP-19		54,000 45,000	
Enamelysin ³	MMP-20		54,000 22,000	
Nonmammalian				
<i>Xenopus</i> XMMP ⁴			70,000 53,000	Cys in catalytic domain
Envelysin ⁵			63,000 48,000	Sea urchin
Soybean MMP ⁶			? 19,000	Protein sequencing

Note: The values of *M_r*, except for MMP-3, are based on cDNA sequence; glycosylation may increase these values. Values for the active forms of MT-MMPs assume cleavage at the furin site. Names in bold are those recommended by the IUBMB. Certain of these enzymes do not receive further attention in this individual chapter; reference to these is as follows: ¹ Basset *et al.*, 1990; ² Cozzini *et al.*, 1998; Pendas *et al.*, 1997; ³ Bartlett *et al.*, 1996; ⁴ Yang *et al.*, 1997; ⁵ Lepage and Gache, 1990; ⁶ McGeehan *et al.*, 1992.

Fig. 15

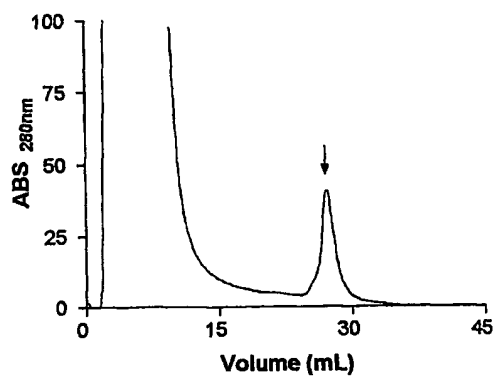


Fig. 16A

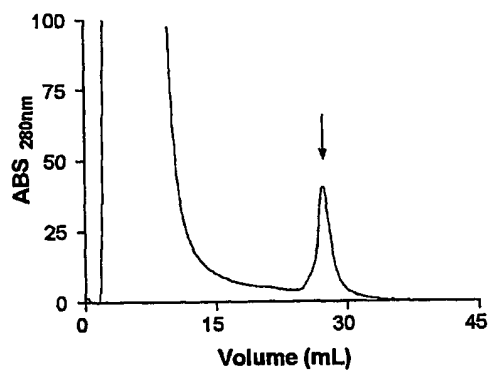


Fig. 16B

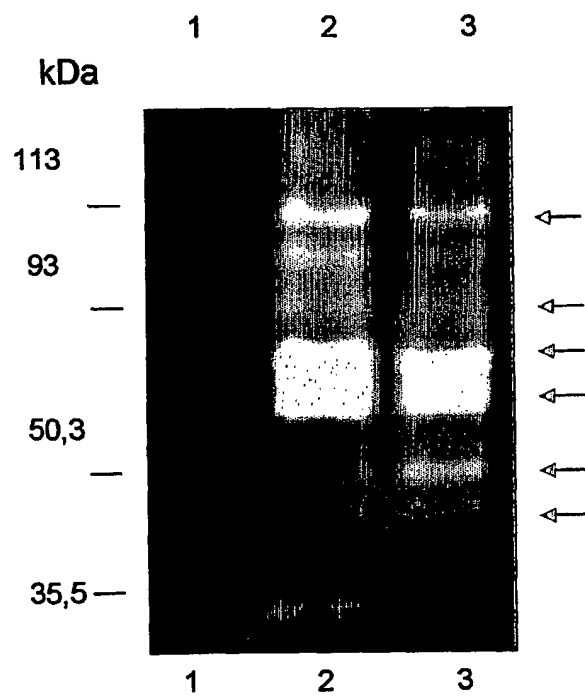


Fig. 17

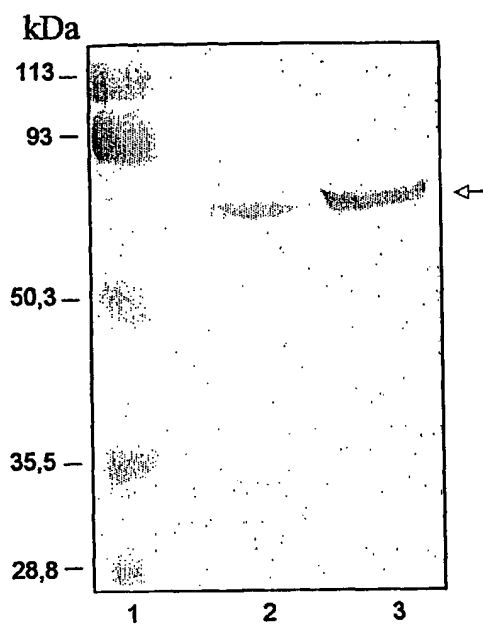


Fig. 18A

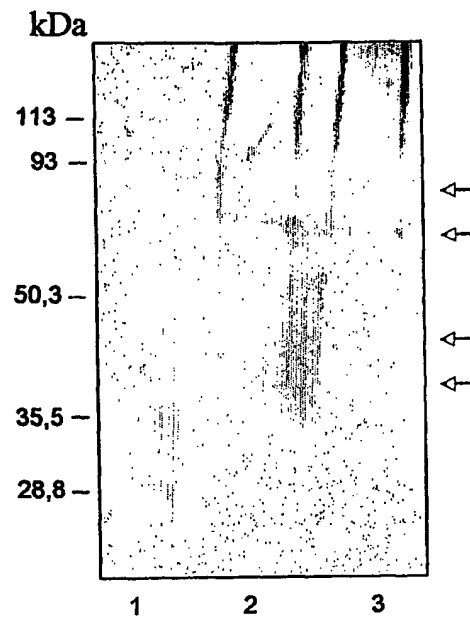


Fig. 18B

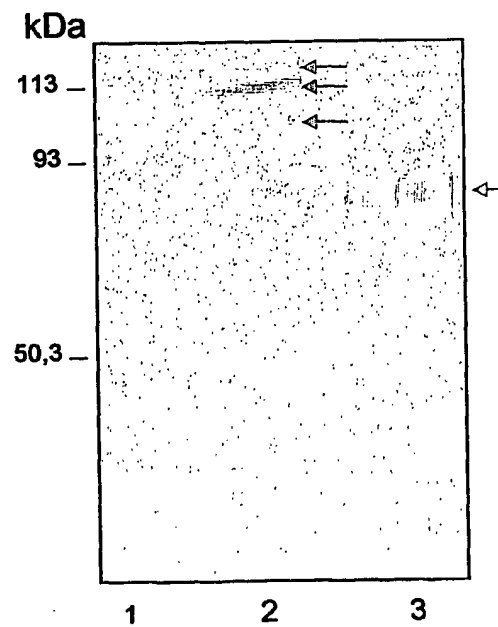


Fig. 18C

kDa

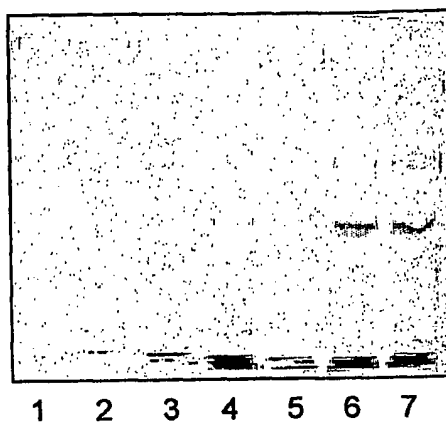


Fig. 19A

kDa

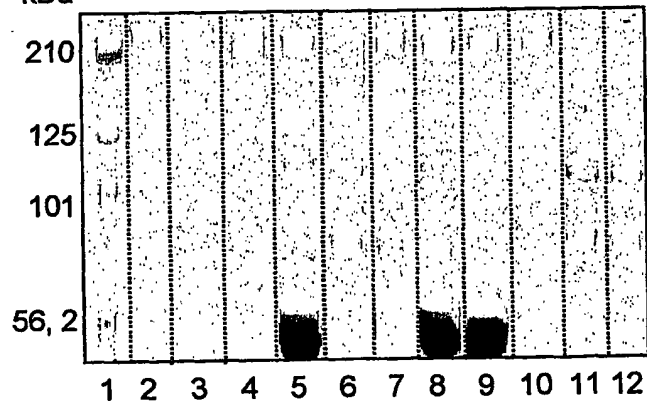


Fig. 19B

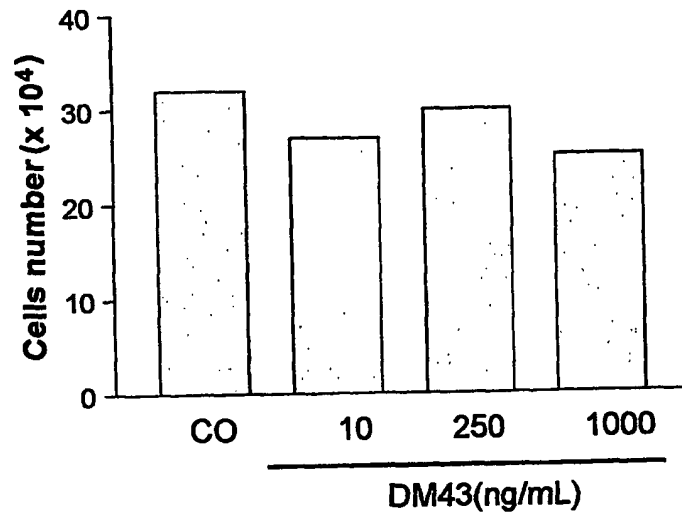


Fig. 20

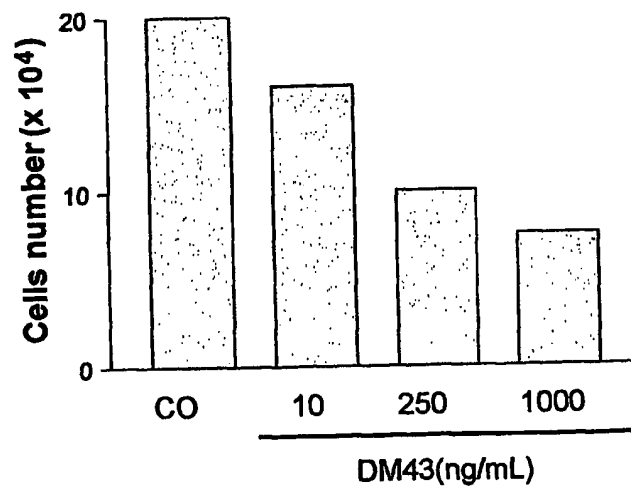


Figura 21

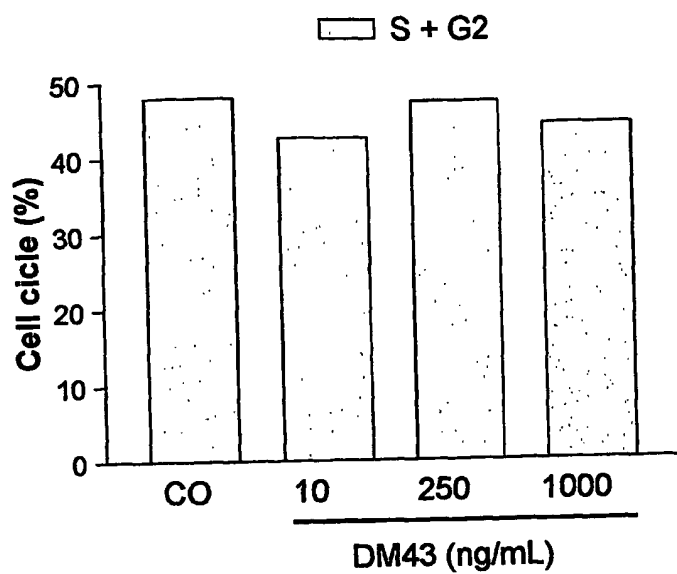


Fig. 22

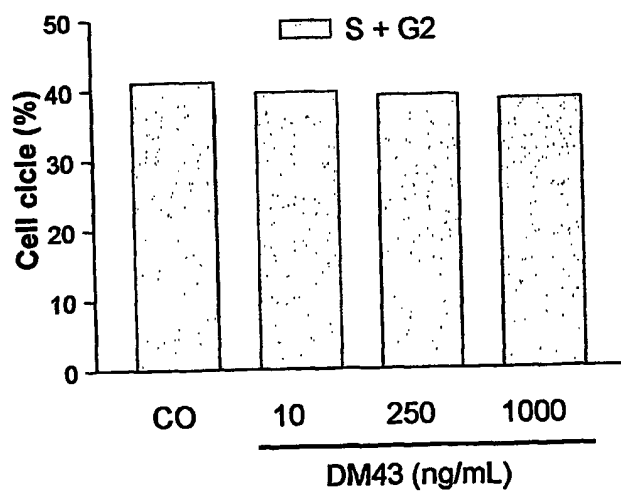


Fig. 23

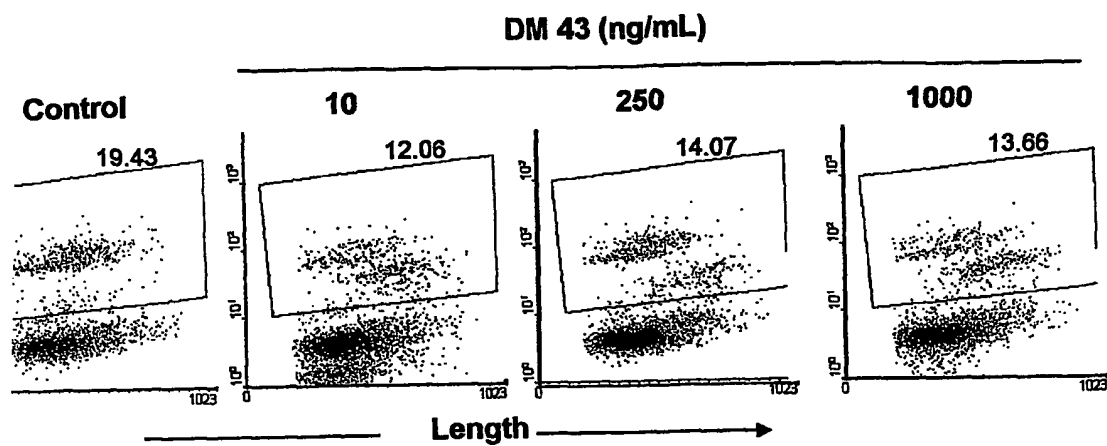


Fig. 24A

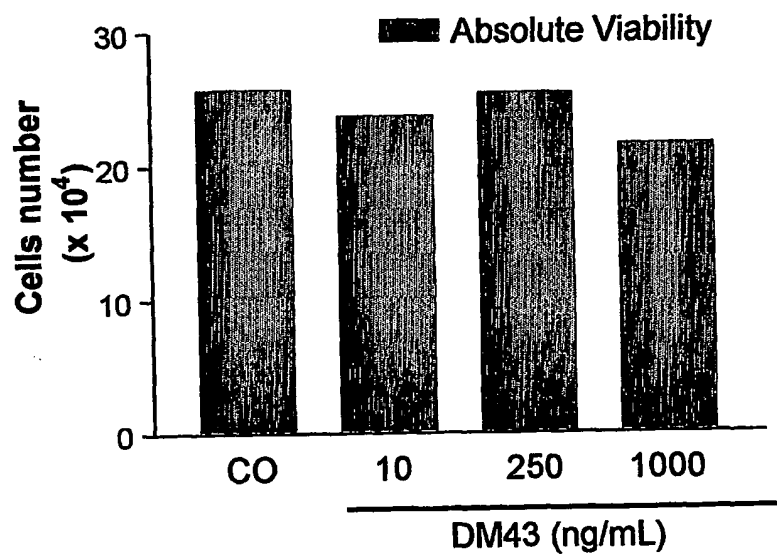


Fig. 24B

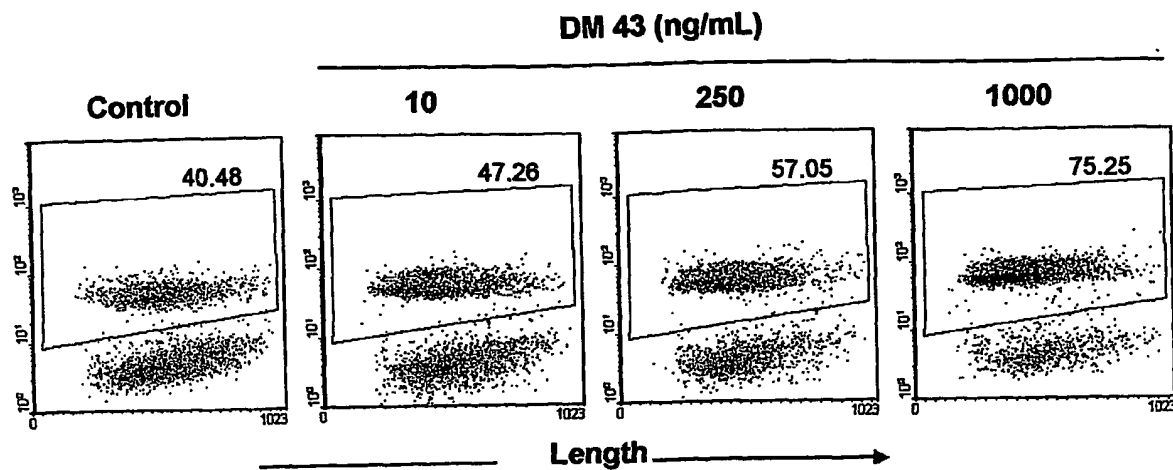


Fig. 25A

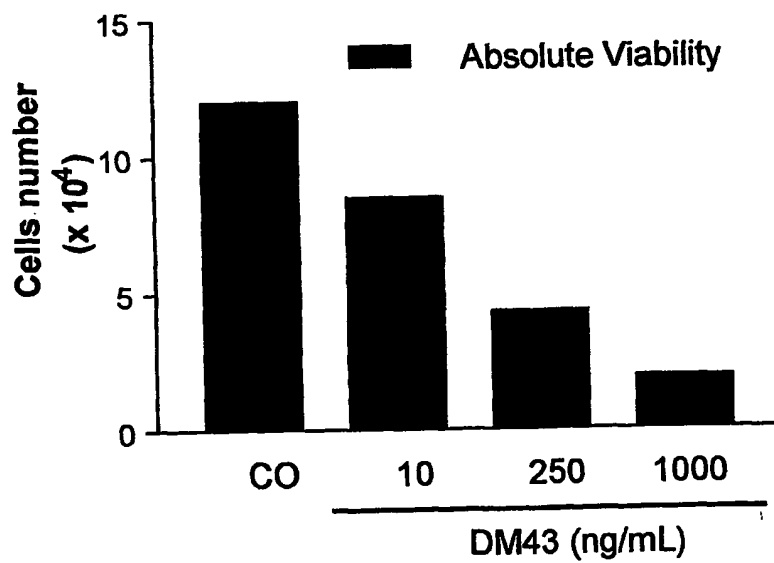


Fig. 25B

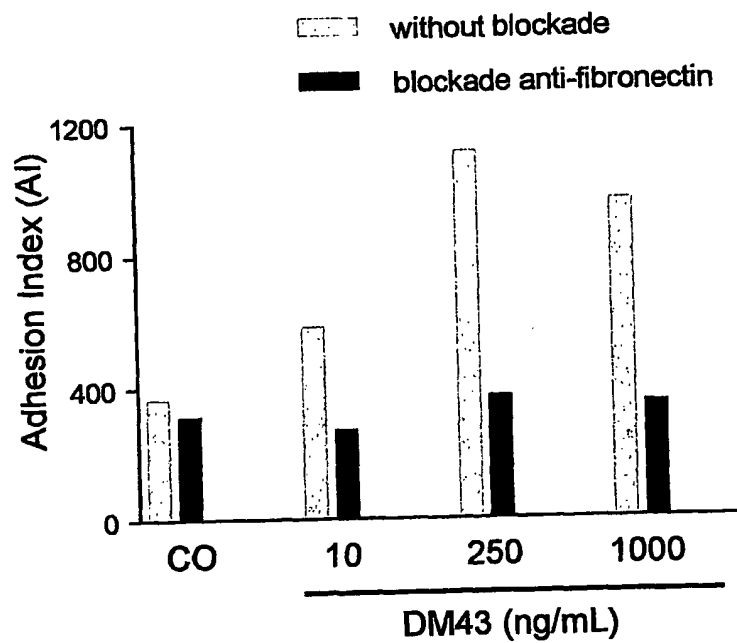


Fig. 26